

Please amend the Specification as follows:

In paragraph 0006 insert the sentences:

[0006] Specifically, discovering functionally similar genes is an important aspect of drug discovery as well as disease diagnosis. Examples appear in U.S. Patent 6,436,642 issued August 20, 2002 and U.S. Patent 6,406,853 issued June 18, 2002. These references are hereby incorporated by reference. Current methods of discovering functional similarity in genes use only the intensity of expression. However, the intensity of gene expression can vary with time and follows a specific pattern. For example, progression through the eukaryotic cell cycle is known to be both regulated and accompanied by characteristic periodic fluctuations in the expression levels of numerous genes.

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In paragraph 0039 insert the sentence:

[0039] The program product of the invention also has means at block 225 for removing a first gene from a cluster cb when the first gene is also in another cluster ca which has another gene with a higher match fraction with the first gene than any of the genes in the cluster cb have with the first gene. When a gene has such a higher match fraction mf with another gene in another cluster ca but the difference between the match fractions is less than a predetermined match difference threshold mdt value such as 5 percent, and the similarity with the other gene comprises more subsequences than the similarity in the cluster cb, then the gene is placed only in the cluster cb and is removed from the another cluster ca. In other words, a first gene expression profile is removed from a cluster when another cluster has another gene expression profile with a higher match fraction with the first gene expression profile, unless the another gene expression profile requires a larger number of subsequences to achieve similarity with the first gene expression profile. This programmed logic removing means is cycled until all genes are listed in only one cluster.

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